# IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Applica	ition of:	)  Group Art Unit: Not Assigned
	Elaine Weidenhammer et al.	)  Examiner: Not Assigned
Serial No.:	Not Assigned	) )
Filed:	Herewith	) )
For: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MICROASSAYS		) ) )

### PRELIMINARY AMENDMENT

BOX Patent Application Commissioner for Patents Washington, D.C. 20231

Sir:

Prior to examination of the subject application, please amend same as follows:

## IN THE SPECIFICATION:

Please amend the Title to read as follows:

# PRIMER EXTENSION DETECTION METHODS ON ACTIVE ELECTRONIC MICROARRAYS

Please insert the following paragraph on page 1, after the Title:

-- This application is a divisional of co-pending U.S. Patent Application Serial Number 09/710,200, filed on November 9, 2000, and is also a continuation-in-part of co-pending oc-93607.1

CERTIFICATE OF MAILING (37 C.F.R. §1.10)

I hereby certify that I have a reasonable basis to expect that this paper (along with any referred to as being attached or enclosed) is being deposited with the U.S. Postal Service on the date shown below with sufficient postage as 'Express Mail - Post Office To Addressee' in an envelope addressed to Commissioner for Patents, Washington, DC 20231.

Express Mail Label No.: EL622500755US Date of Deposit: February 12, 2002

Micheal A. Smith

U.S. Patent Application Serial Number 09/490,965, filed on January 24, 2000, which is a continuation of U.S. Patent Application Serial Number 08/271,882, filed July 7, 1994, now U.S. Patent Number 6,017,696. —

Please replace Table 2 on pages 31-36 with the following Table:

TABLE 2
Oligonucleotides Used in the Above Experimental Procedures,
Organized by Target Gene

Target Gene	Primer name and description	Primer sequence
Angiotensinogen	bAt7AngBpm.s1— biotinylated chimeric T7 promoter/gene specific oligonucleotide	BiotinTAATACGACTCACTATAGG GAGACACAGAACTGGATGTTGC TGCTGGAG [SEQ. ID NO. 1]
Angiotensinogen	cAng.a1—capture for RNA	BiotinCATGAACCTGTCAATCTTCT [SEQ. ID NO. 2]
Angiotensinogen	pAng.a1—3' gene specific primer	GGAAGGTGCCCATGCCAGAGA [SEQ. ID NO. 3]
Cathepsin G	bAt7CathBpm.s1— biotinylated chimeric T7 promoter/gene specific oligonucleotide	BiotinTAATACGACTCACTATAGG GAGAGCTGCCTTCAAGGGGGAT TCTGGAG [SEQ. ID NO. 4]
Cathepsin G	pCath.a1—3' gene specific primer	AGCTTCTCATTGTTGTCCTTATC C [SEQ. ID NO. 5]
Cathepsin G	cCath.a1—capture for RNA	BiotinTGTTACACAGCAGGGGGC CT [SEQ. ID NO. 6]
c-jun	bT7jun.s1—biotinylated chimeric T7 promoter/gene specific oligonucleotide	BiotinTAATACGACTCACTATAGG GAGACGGCCAACATGCTCAGGG AACAGGT [SEQ. ID NO. 7]
c-jun	cjun.s1—capture for cDNA	BiotinCAAACATTTTGAAGAGAGA CCGTCG [SEQ. ID NO. 8]
c-jun	pjun.a1—3' gene specific primer	TTTTTCTTCGTTGCCCCTCAGCC [SEQ. ID NO. 9]
COX1	pcox1.as.3 —gene specific primer for generation of 500bp fragment	TGCCCAGGATTGATTCACAGG [SEQ. ID NO. 10]

Target Gene	Primer name and	Primer sequence
001/4	description	AGGCCAGAAGGAATGATGGG
COX1	pcox1.as.2—gene	[SEQ. ID NO. 11]
	specific primer for	[SEQ. ID NO. 11]
	generation of 250bp	
	fragment	CTAAGCCCAAAGTGTGGATC
COX1	pcox1.as.1—gene	[SEQ. ID NO. 12]
	specific primer for	[SEQ. ID NO. 12]
	generation of 100bp	
	fragment	
COX1	T7.cox1.s—chimeric	GAAATTAATACGACTCACTATAG
	T7/gene specific	GGAGAACCCTTTTCTCAGGACCT
	oligonucleotide	CTGGAGG [SEQ. ID NO. 13]
COX1	cCOX1bpm.a1—capture	BiotinACAGAGGTCCTGAGAAAAG
	for RNA	GGTCT [SEQ. ID NO. 14]
COX2	bAt7COX2bpm.s2—	BiotinTAATACGACTCACTATAGG
	biotinylated chimeric T7	GAGACTATGAATCATTTGAAGAA
	promoter/gene specific	CTTACTGGAG [SEQ. ID NO. 15]
	oligonucleotide	
COX2	cCOX2.a2—capture for	BiotinCTGCAGACATTTCCTTTTCT
	RNA	[SEQ. ID NO. 16]
COX2	pCOX2.a2—3' gene	GCATCTGGCCGAGGCTTTTCTAC
* :	specific primer	[SEQ. ID NO. 17]
GAPDH	pGAPs.2—gene specific	GTTCGACAGTCAGCCGCATCTTC
	primer for generation of	[SEQ. ID NO. 18]
	500 bp fragment	
GAPDH	pGAPs.3—gene specific	TGATGCCCCCATGTTCGTCATGG
	primer for generation of	[SEQ. ID NO. 19]
	100 bp fragment	
GAPDH	pGAPs.4—gene specific	CTTCCAGGAGCGAGATCCCTCC
	primer for generation of	[SEQ. ID NO. 20]
	250 bp fragment	
GAPDH	T7GAPbpm.a1—chimeric	GTAATACGACTCACTATAGGGCG
	T7/gene specific	GGGTGCTAAGCAGTTGGTGGTG
e e e	oligonucleotide	CTGGAG [SEQ. ID NO. 21]
GAPDH	cGAPbpm.s1—capture	BiotinCAGCCTCAAGATCATCAGC
	for aRNA	AATGCCT [SEQ. ID NO. 22]
GAPDH	bAt7GAPbpm.s2—	BiotinTAATACGACTCACTATAGG
	biotinylated chimeric T7	GAGACTCAAGGGCATCCTGGGC
	promoter/gene specific	TACACTGGAGCAC [SEQ. ID NO.
	oligonucleotide	23]
GAPDH	pGAPDH.a6—3' gene	GAGGTCCACCACCCTGTTGCTG
J, (1 D) 1	specific primer	TAG [SEQ. ID NO. 24]

Target Gene	Primer name and	Primer sequence
O L DDI	description	BiotinGTTGAAGTCAGAGGAGACC
GAPDH	cGAPbpm.a2—capture for RNA	ACCTGGTGCT [SEQ. ID NO. 25]
1310.47	bAt7HMG17Bpm.s1—	BiotinTAATACGACTCACTATAGG
HMG-17		GAGAGGAATAACCCTGCAGAAA
	biotinylated chimeric T7	CTGGAG [SEQ. ID NO. 26]
	promoter/gene specific	C 100A0 [SEQ: 15 140: 20]
1040 47	oligonucleotide	CCCTTCCCCCAAAAACAACAATG
HMG-17	pHMG17.a1—3' gene	A [SEQ. ID NO. 27]
LIN4O 47	specific primer	BiotinCCTGGTCTGTTTTGGCATC
HMG-17	cHMG17.a1—capture for RNA	T [SEQ. ID NO. 28]
1 1 1 1 2		ATTCTGCCCTCGAGCCCACCGG
Interleukin 6	pIL6s.4—gene specific	G [SEQ. ID NO. 29]
	primer for generation of	G [SEQ. ID NO. 29]
1 1 1 2	500bp fragment	CAAACAAATTCGGTACATCCTCG
Interleukin 6	plL6S.3—gene specific	[SEQ. ID NO. 30]
	primer for generation of	
1 1 1 2	250bp fragment	TGGATTCAATGAGGAGACTTGCC
Interleukin 6	pIL6S.2—gene specific	[SEQ. ID NO. 31]
	primer for generation of	[320. 10 140. 31]
lata da dia C	100bp fragment T7IL6bpm.a1—chimeric	GTAATACGACTCACTATAGGGCG
Interleukin 6	T7/gene specific	CCTCACTACTCTCAAATCTGTTC
,	oligonucleotide	TGGAG [SEQ. ID NO. 32]
Interleukin 6	clL6bpm.s1—capture for	BiotinGGAGTTTGAGGTATACCTA
Interieukin	aRNA	GAGTACCT [SEQ. ID NO. 33]
Interleukin 6	bT7IL6.s1—biotinylated	BiotinTAATACGACTCACTATAGG
interieukin o	chimeric T7	GAGACCTGAGGGCTCTTCGGCA
	promoter/gene specific	AATGTAG [SEQ. ID NO. 34]
	oligonucleotide	70 (10 1) (0 [02 0.10 1.10 1.10 1.10 1.10 1.10 1.10 1.
Interleukin 6	clL6.s1—capture for	BiotinAATGGGCATTCCTTCT
Interiodian o	cDNA	GGTCAG [SEQ. ID NO. 35]
Interleukin 6	pll6.a1—3' gene specific	GAACAACATAAGTTCTGTGCCCA
III.CHOUKIII O	primer	GTG [SEQ. ID NO. 36]
Interleukin 1 beta	bT7IL1.s1—biotinylated	BiotinTAATACGACTCACTATAGG
Intollouidi i bota	chimeric T7	GAGACAGAAAACATGCCCGTCTT
	promoter/gene specific	CCTGG [SEQ. ID NO. 37]
	oligonucleotide	
Interleukin 1 beta	clL1.s1—capture for	BiotinGCGGCCAGGATATAACTGA
	cDNA	CTTCAC [SEQ. ID NO. 38]
Interleukin 1 beta	pll1.a1—3' gene specific	TCCACATTCAGCACAGGACTCTC
	primer	TG [SEQ. ID NO. 39]

Target Gene	Primer name and description	Primer sequence
LD70	bAt7LD78Bpm.s1—	BiotinTAATACGACTCACTATAGG
LD78	biotinylated chimeric T7	GAGAAGTGACCTAGAGCTGAGT
	promoter/gene specific	GCCTGGAG [SEQ. ID NO. 40]
	oligonucleotide	000,00,10 [2241.2741]
LD78	pLD78.a1—3' gene	CTCTCAGAGCAAACAATCACAAA
LUIO	specific primer	CACAC [SEQ. ID NO. 41]
I D70	cLD78.a1—capture for	BiotinTCGAAGCTTCTGGACCCCT
LD78	RNA	[SEQ. ID NO. 42]
Ostoppontin	bAt7OstBpm.s1—	BiotinTAATACGACTCACTATAGG
Osteopontin	biotinylated chimeric T7	GAGAGAGGTGATAGTGTGGTTT
	promoter/gene specific	ATGGACTGGAG [SEQ. ID NO. 43]
	oligonucleotide	7,1,00,10,00,10 [0_0,00]
Osteopontin	pOst.a1—3' gene specific	CAACGGGGATGGCCTTGTATGC
Osteopontin	primer	[SEQ. ID NO. 44]
Ostoonontin	cOst.a1—capture for	BiotinAACTTCTTAGATTTTGACCT
Osteopontin	RNA	[SEQ. ID NO. 45]
-52	pp53s.3—gene specific	ACAGAAACACTTTTCGACATAG
p53	primer for generation of	[SEQ. ID NO. 46]
	500bp fragment	[
p53	pp53s.2—gene specific	AAAGGGAGCCTCACCACGAGC
ροσ	primer for generation of	[SEQ. ID NO. 47]
	250bp fragment	
p53	pp53.s1—gene specific	CGTGAGCGCTTCGAGATGTTCC
poo	primer for generation of	[SEQ. ID NO. 48]
	100bp fragment	
p53	T7p53bpm.a1—chimeric	GTAATACGACTCACTATAGGGCG
poo	T7/gene specific	ACCCTTTTTGGACTTCAGGTGGC
	oligonucleotide	TGGAG [SEQ. ID NO. 49]
p53	cp53bpm.s1—capture for	BiotinGAGCCAGGGGGGGAGCAGG
Poo	aRNA	GCTCACT [SEQ. ID NO. 50]
TGFβ1	pTGFb1S.3—gene	GGGATAACACACTGCAAGTGGA
101 p1	specific primer for	C [SEQ. ID NO. 51]
	generation of 500bp	
	fragment	
TGFβ1	pTGFb1s.2—gene	CCACGAGCCCAAGGGCTACCAT
10. p.	specific primer for	GC [SEQ. ID NO. 52]
	generation of 250bp	
	fragment	
TGFβ1	pTGFb1.s1—gene	CGCTGGAGCCGCTGCCCATCGT
	specific primer for	GTA [SEQ. ID NO. 53]
	generation of 100bp	
	fragment	

Target Gene	Primer name and	Primer sequence
rarget cono	description	
TGFβ1	T7TGFb1bpm.a1—	GTAATACGACTCACTATAGGGCG
1 Gi pi	chimeric T7/gene specific	GGCGGGACCTCAGCTGCACTTG
	oligonucleotide	CTGGAG [SEQ. ID NO. 54]
TGFβ1	cTGFb1bpm.s1—capture	BiotinCAGCTGTCCAACATGATCG
ТОГР	for aRNA	TGCGCT [SEQ. ID NO. 55]
TGFβ2	bT7TGFb.s1—	BiotinTAATACGACTCACTATAGG
Ι ΟΙ, β2	biotinylated chimeric T7	GAGACTCTGCCTCCTGCCT
	promoter/gene specific	GTCTGC [SEQ. ID NO. 56]
	oligonucleotide	
TGFβ2	cTGFb.s1—capture for	BiotinCGGCATCAAGGCACAGGG
101 p2	cDNA	GACCAGT [SEQ. ID NO. 57]
TGFβ2	pTGFb.a1—3' gene	CTTCAACAGTGCCCAAGGTGCT
1 Or pz	specific primer	CAA [SEQ. ID NO. 58]
TPOX	TPOX9C—biotinylated	BiotinTTAGGGAACCCTCACTGAA
11.0%	synthetic target	TGAATGAATGAATGAATGA
	3,	ATGAATG [SEQ. ID NO. 59]
TPOX	TPOXcapcomp—Cy3	CATTCATTCAGTGAGGGTT
11.0%	labeled reporter for	CC [SEQ. ID NO. 60]
	TPOX9C	
Vimentin	bAt7VimBpm.s2—	BiotinTAATACGACTCACTATAGG
	biotinylated chimeric T7	GAGACATCGACAAGGTGCGCTT
	promoter/gene specific	CCTGGAG [SEQ. ID NO. 61]
	oligonucleotide	
Vimentin	pVim.a1—3' gene	CGCGGCTTTGTCGTTGGTTAG
	specific primer	[SEQ. ID NO. 62]
Vimentin	cVim.a2—capture for	BiotinCAGGATCTTATTCTGCTGC
	RNA	T [SEQ. ID NO. 63]
β-Actin	bAt7Actin.s—biotinylated	BiotinTAATACGACTCACTATAGG
	chimeric T7	GAGACCCCTTTTTGTCCCCCAAC
	promoter/gene specific	TGGAGA [SEQ. ID NO. 64]
	oligonucleotide	
β-Actin	cActin.a—capture for	BiotinCCAAAAGCCTTCATACATC
1	RNA	T [SEQ. ID NO. 65]
β-Actin	pbAa.4—3' gene specific	AAGGTGTGCACTTTTATTCAACT
•	primer	GGTCTCAAG [SEQ. ID NO. 66]
β-la	pT7AmpBpm.s1—	TAATACGACTCACTATAGGCTGG
•	chimeric T7/gene specific	
	oligonucleotide for	GAG [SEQ. ID NO. 67]
	generation of short RNA	
β-la	pAmp.a2—3' primer with	T <sub>30</sub> CCAATGCTTAATCAGTGAGGC
	poly(dT) tract	ACCTATCTC [SEQ. ID NO. 68]

Target Gene	Primer name and description	Primer sequence
β-la	cAmp.a1—capture for RNA	biotin- CGAGACCCACGCTCACCGGCT [SEQ. ID NO. 69]
β-lа	pT7Amp.s1—chimeric T7/gene specific oligonucleotide for generation of full-length gene	TAATACGACTCACTATAGGGCAC CCAGAAACGCTGGTGAAAGTAA AAG [SEQ. ID NO. 70]
β- Thromboglobulin- like protein gene	bAt7Throm.s1— biotinylated chimeric T7 promoter/gene specific oligonucleotide	BiotinTAATACGACTCACTATAGG GAGAGGAAAACTGGGTGCAGAG GGTTCTGGAG [SEQ. ID NO. 71]
β- Thromboglobulin- like protein gene	pbThrom.a1—3' gene specific primer	GGCAACCCTACAACAGACCCAC AC [SEQ. ID NO. 72]
β- Thromboglobulin- like protein gene	cbThrom.a1—capture for RNA	BiotinAGCCCTCTTCAAAAACTTCT [SEQ. ID NO. 73]

After page 36, and before the claims, please insert the <u>Sequence Listing</u>, attached hereto as Appendix "A".

Please replace the abstract on page 46 with the following abstract paragraph:

The present invention presents techniques useful in methods for gene expression monitoring, and other nucleic acid hybridization assays, that utilize microelectronic arrays to drive the transport and hybridization of nucleic acids. Particularly, methods for detecting the level of sample amplicons using electronically assisted primer extension detection, and utilizing individual test site hybridization controls are provided by the present invention. These methods are particularly useful for hybridization assays in which a plurality of nucleic acids are being assayed, as they eliminate the need for the hybridization of multiple reporter probes to captured nucleic acids on the active electronic microarray.

### IN THE CLAIMS

Please cancel, without prejudice to their prosecution in another application, claims 1-53 and 59-72.

Please add new claims 73-88:

73. A method of detecting the extent of hybridization of a plurality of nucleic acids in a sample to a plurality of nucleic acid probes, the method comprising:

- (a) electronically hybridizing the nucleic acid in the sample to a plurality of nucleic acid probes bound to a support at a two or more predetermined locations, wherein:
- i) the nucleic acids in the sample are electronically hybridized to nucleic acid probes at two or more locations on the support, and
- ii) the sequence of at least one nucleic acid probe on a first location is different from the sequence of the nucleic acid probes on a second location.
- (b) utilizing the hybridized nucleic acids as a templates in a nucleic acid polymerase reaction to extend the bound probes, whereby a labeled nucleotide is incorporated into the extended probes; and
- (c) detecting the labeled nucleotide incorporated into the extended bound probes at the predetermined location.
- 74. The method of claim 73 wherein the labeled nucleotide comprises a labeling moiety selected from the group consisting of fluorescent moieties, colorigenic moieties, chemiluminescent moieties, and affinity moieties.
- 75. The method of claim 74 wherein the labeled nucleotide comprises a fluorescent moiety.
- 76. The method of claim 73 wherein the fluorescent moiety is selected from the group consisting of cyanine dye moieties, Bodipy Texas Red moieties, rhodamine moieties, fluorescein moieties, and cumarin moieties.

- 77. The method of claim 76 wherein the fluorescent moiety is a cyanine dye moiety selected from the group consisting of Cy5 and Cy3.
- 78. The method of claim 73 wherein the nucleic acid polymerase reaction is a DNA polymerase reaction.
- 79. The method of claim 73 wherein the nucleic acid polymerase reaction is a reverse-transcriptase reaction.
- 80. The method of claim 73 wherein the two or more locations each comprise at least one nucleic acid probe with the same sequence.
- 81. The method of claim 80 wherein the nucleic acid probe with the same sequence is a control sequence probe.
- 82. The method of claim 73 wherein the nucleic acids in the sample are electronically hybridized to nucleic acid probes at five or more locations on the support, and the sequence of at least one nucleic acid probe at each of the five locations is different from the sequences of the nucleic acid probes at the other locations.
- 83. The method of claim 73 wherein the nucleic acids in the sample are electronically hybridized to nucleic acid probes at ten or more locations on the support, and the sequence of at least one nucleic acid probe at each of the ten locations is different from the sequences of the nucleic acid probes at the other locations.
- 84. The method of claim 73 wherein the nucleic acids in the sample are electronically hybridized to nucleic acid probes at twenty or more locations on the support, and the sequence of at least one nucleic acid probe at each of the twenty locations is different from the sequences of the nucleic acid probes at the other locations.
- 85. The method of claim 73 wherein the nucleic acids in the sample are electronically hybridized to nucleic acid probes at forty or more locations on the support, and the sequence of at least one nucleic acid probe at each of the forty locations is different from the sequences of the nucleic acid probes at the other locations.

The method of claim 54 wherein a control sequence probe is also bound to 86. the support at the location.

- The method of claim 56 wherein the fluorescent moiety is selected from the group consisting of cyanine dye moieties, Bodipy Texas Red moieties, rhodamine moieties, fluorescein moieties, and cumarin moieties.
- The method of claim 87 wherein the fluorescent moiety is a cyanine dye 88. moiety selected from the group consisting of Cy5 and Cy3.

#### **REMARKS**

Applicants have filed this divisional application off of parent application 09/710,200 in order to pursue the subject matter of claims 54-58, which were subject to a restriction requirement in the parent. Applicants have added new claims 73-88 in order to claim further embodiments of this subject matter. Due to the cancellation of claims 1-53 and 59-72, Ling Wang has been removed as an inventor on this divisional application, leaving Elaine Weidenhammer, Xiao Xu, Michael Heller, and Brenda Kahl as inventors.

Applicants submit herewith a paper Sequence Listing and computer readable copy in compliance with 37 CFR 1.821 through 1.825. The Sequence Listing adds no new matter to the application, and the computer readable copy is identical to the paper copy. References to the Sequence ID Numbers in the application have been added to the specification by the above amendment, as has the paper copy of the Sequence Listing.

If the Examiner has any questions regarding this Application or the Preliminary Amendment, he is invited to contact the undersigned at (949) 567-2305.

Respectfully submitted,

LYON & LYON LLP

Dated: February 12, 2002

Patrick S. Eagleman Reg. No. 44,665

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